Figure 1

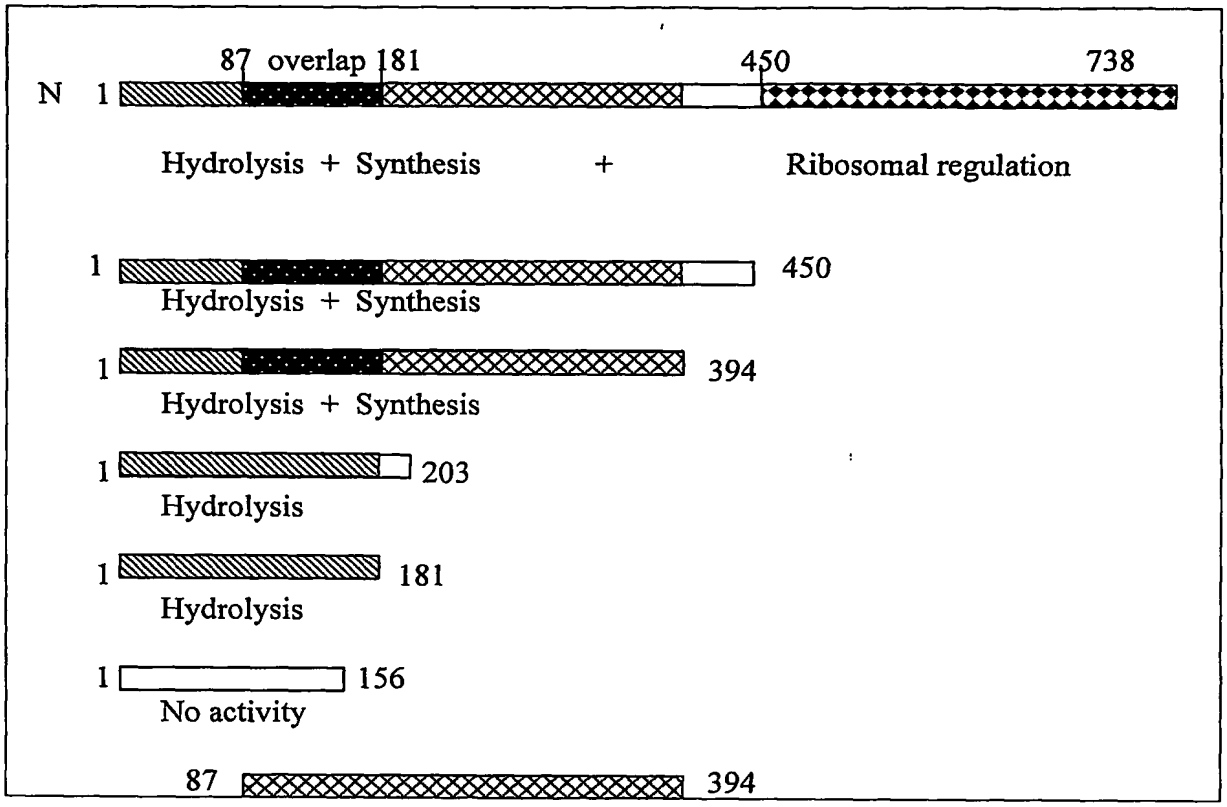
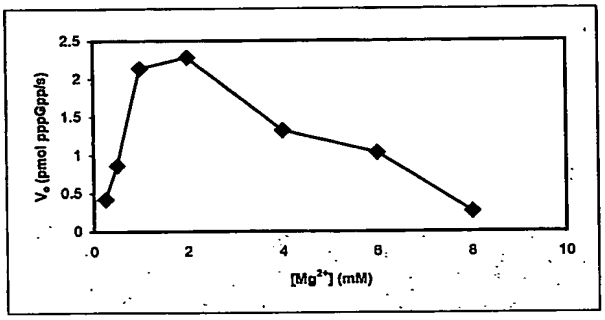

87 overlap 181
450
738
N 1
Hydrolysis + Synthesis + Ribosomal regulation
1
450
Hydrolysis + Synthesis
1
394
Hydrolysis + Synthesis
1
203
Hydrolysis
1
181
Hydrolysis
1
156
No activity
87
394

FIGURE 2

A



B

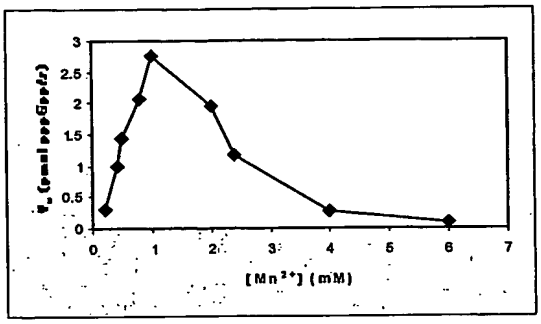
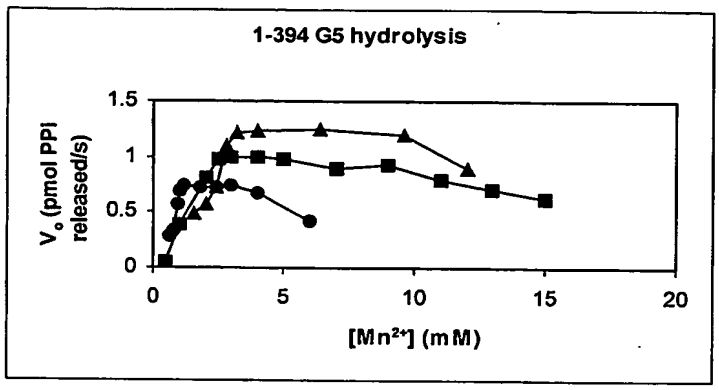
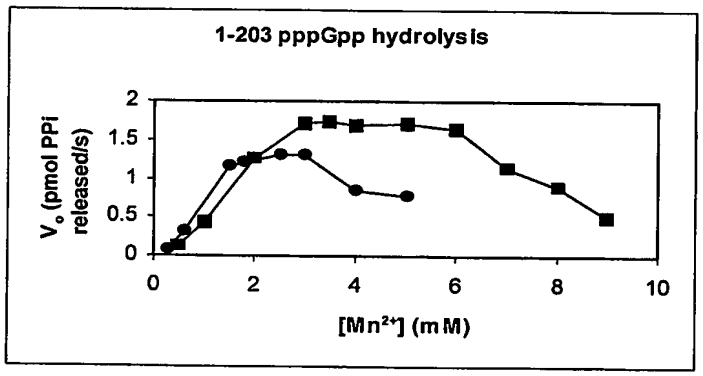


FIGURE 3

A


1-394 G5 hydrolysis
V_o (pmol PPi released/s)
1.5
1
0.5
0
0
5
10
15
20
[Mn2+] (mM)

B


1-203 pppGpp hydrolysis
V_o (pmol PPi released/s)
2
1.5
1
0.5
0
0
2
4
6
8
10
[Mn2+] (mM)

C

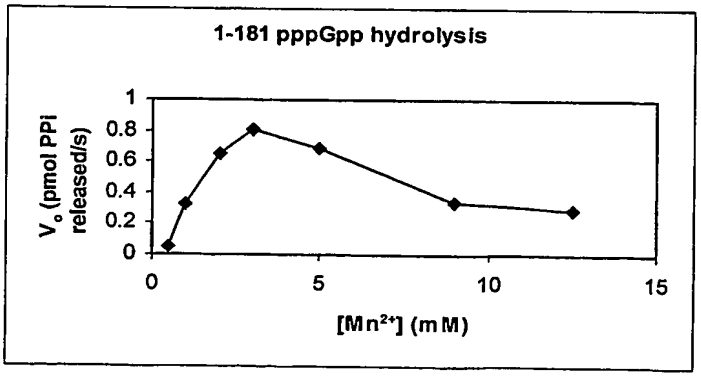
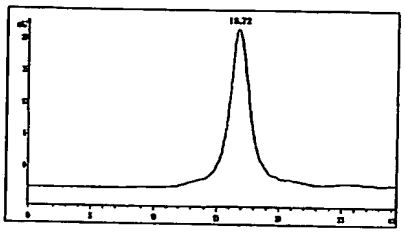
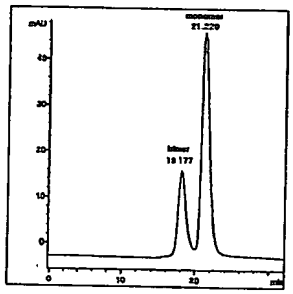

1-181 pppGpp hydrolysis
V_o (pmol PPi released/s)
1
0.8
0.6
0.4
0.2
0
0
5
10
15
[Mn2+] (mM)

FIGURE 4

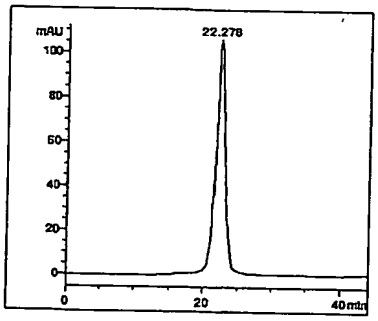
A



B



C.



D

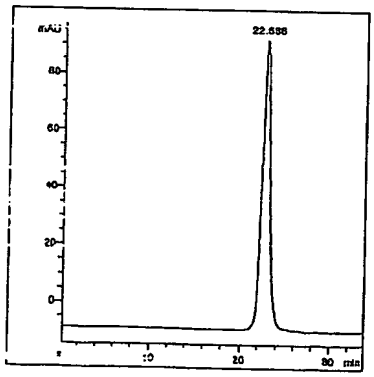


Figure 5

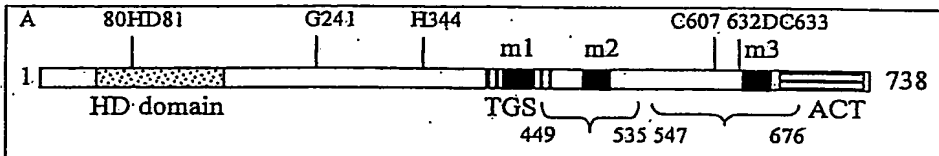
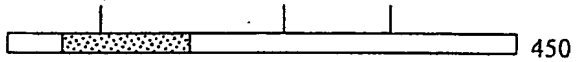
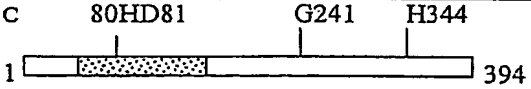
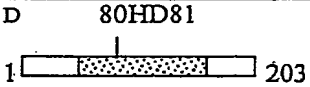
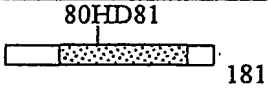
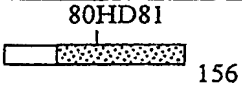
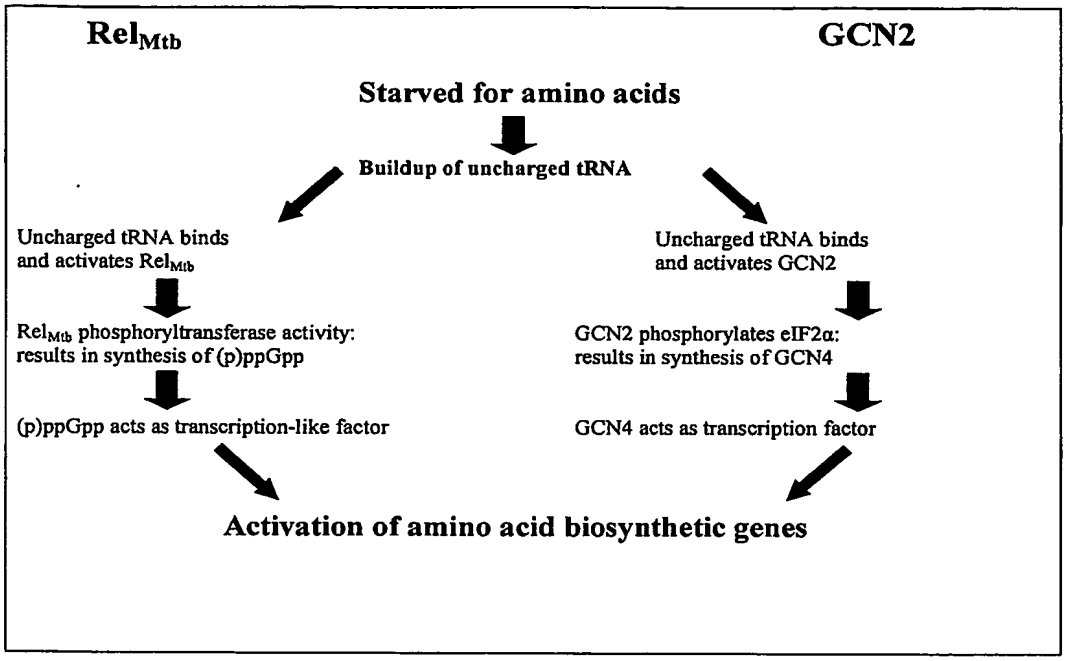
A 		•TGS 396-459 (*21*) •ACT 661-734 (*22*) •m1 (413-442), m2 (481-514), m3 (634-651) motifs •449-535 & 547-676 multimer area (*20*) •C607, D632, C633 multimer residues (*16*) •449-C term. ribosome binding (*20*)
B 	Synthesis & Hydrolysis	•G241 and H344 for probable nucleotide binding (*16*) •HD domain and doublet (*13*)
C 	Synthesis & Hydrolysis	•G241 and H344 for probable nucleotide binding (*16*) •HD domain and doublet (*13*)
D 	Hydrolysis	•HD domain and doublet (*13*) •Lacks probable ATP and GTP binding sites
E 	Hydrolysis	•HD domain and doublet (*13*) •Lacks probable ATP and GTP binding sites
F 	No detectable activity	•HD doublet present but HD domain disrupted
G 	Synthesis	•No HD doublet and disrupted HD domain •G241 and H344 for probable ATP and GTP binding (*16*)

FIGURE 6


Rel$_{Mtb}$
GCN2
Starved for amino acids
Buildup of uncharged tRNA
Uncharged tRNA binds and activates Rel$_{Mtb}$
Uncharged tRNA binds and activates GCN2
Rel$_{Mtb}$ phosphoryltransferase activity: results in synthesis of (p)ppGpp
GCN2 phosphorylates eIF2α: results in synthesis of GCN4
(p)ppGpp acts as transcription-like factor
GCN4 acts as transcription factor
Activation of amino acid biosynthetic genes